

## WEST Search History

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DATE: Wednesday, March 21, 2007

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L4	L3 and activity	229
<input type="checkbox"/>	L3	hepatoma derived growth factor	244
		<i>DB=USPT; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L2	L1 and hdgf	42
<input type="checkbox"/>	L1	hepatoma derived growth factor	49

END OF SEARCH HISTORY

d his

(FILE 'HOME' ENTERED AT 10:39:50 ON 21 MAR 2007)

FILE 'MEDLINE, EMBASE, BIOSIS' ENTERED AT 10:40:06 ON 21 MAR 2007

L1	173 S HDGF
L2	31 S L1 AND RAT
L3	17 DUPLICATE REMOVE L2 (14 DUPLICATES REMOVED)
L4	29052 S HRP
L5	197 S HEPATOMA DERIVED GROWTH FACTOR
L6	29 S L5 AND HUH-7
L7	11 DUPLICATE REMOVE L6 (18 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 10:42:33 ON 21 MAR 2007

FILE 'GENBANK' ENTERED AT 10:49:19 ON 21 MAR 2007

L8	1 S AY061636
L9	1 S BC085707
L10	1 S AF458587
L11	1 S AF458586

Day : Wednesday

Date: 3/21/2007

Time: 08:34:32

 **PALM INTRANET**

## Inventor Information for 10/501053

Inventor Name	City	State/Country
<u>YU, LONG</u>	SHANGHAI	CHINA
<u>TANG, LISHA</u>	SHANGHAI	JAPAN
<u>GUO, ZEKUN</u>	SHANGHAI	CHINA
<u>ZHANG, PINGZHAO</u>	SHANGHAI	CHINA
<u>DONG, YIMIN</u>	SHANGHAI	CHINA

[Appln Info](#)[Contents](#)[Petition Info](#)[Atty/Agent Info](#)[Continuity/Reexam](#)[Foreign E](#)Search Another: Application#   or Patent#  PCT /  /   or PG PUBS #  Attorney Docket #  Bar Code #  

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Day : Wednesday

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## Continuity Information for 10/501053

### Parent Data

10501053is a national stage entry of PCT/CN03/00003 International Filing Date: 01/02/2003

### Child Data

No Child Data

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2006, 19:14:17 ; Search time 5625 Seconds  
(without alignments)  
11254.746 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	966	97.6	2068	6 BC085707	BC085707 Rattus no
2	966	97.6	338115	12 AC111953	AC111953 Rattus no
3	924.4	93.4	1512	6 AY061636	AY061636 Rattus no
4	907.4	91.7	909	5 AF458587	AF458587 Homo sapi
5	885.4	89.4	921	6 AF458586	AF458586 Rattus no
6	572.6	57.8	2046	6 BC108388	BC108388 Mus muscu

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c	8	572.6	57.8	204891	12	AL837519	AL837519 Mus muscu
	9	571	57.7	1332	2	E14400	E14400 cDNA encodi
	10	571	57.7	1333	6	D63663	D63663 Mus musculu
	11	511.8	51.7	870	5	AF451983	AF451983 Homo sapi
	12	503.6	50.9	1856	6	AF180109	AF180109 Mus muscu
	13	347.8	35.1	783	2	E17007	E17007 DNA encodin
	14	276.4	27.9	495	5	AF451984	AF451984 Homo sapi
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	18	226.8	22.9	880	2	AX111704	AX111704 Sequence
	19	226.8	22.9	143429	5	HS309H15	AL033539 Human DNA
	20	222	22.4	2034	5	AK056824	AK056824 Homo sapi
	21	211.6	21.4	2147	14	BC109529	BC109529 Bos tauru
	22	211.6	21.4	188230	12	AC159382	AC159382 Bos tauru
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	28	170.8	17.3	152842	6	AC156500	AC156500 Mus muscu
	29	170	17.2	213866	6	AC114589	AC114589 Mus muscu
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c	35	165.4	16.7	200574	6	BX005304	BX005304 Mouse DNA
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	44	163	16.5	163916	6	AC141887	AC141887 Mus muscu
c	45	162.8	16.4	191753	6	AC125235	AC125235 Mus muscu

## ALIGNMENTS

## RESULT 1

BC085707

LOCUS BC085707 2068 bp mRNA linear ROD 20-OCT-2005

DEFINITION Rattus norvegicus hepatoma-derived growth factor, related protein 1, mRNA (cDNA clone MGC:93218 IMAGE:7132556), complete cds.

ACCESSION BC085707

VERSION BC085707.1 GI:55715911

KEYWORDS MGC.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 2068)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,  
 Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,  
 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,  
 Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,  
 Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,  
 Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,  
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,  
 Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,  
 Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,  
 Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,  
 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,  
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,  
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,  
 Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,  
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

CONSRTM Mammalian Gene Collection Program Team  
 TITLE Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 PUBMED 12477932  
 REFERENCE 2 (bases 1 to 2068)  
 AUTHORS .  
 CONSRTM NIH MGC Project  
 TITLE Direct Submission  
 JOURNAL Submitted (01-NOV-2004) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Howard Jacobs  
 cDNA Library Preparation: Express Genomics  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
 R. M.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 184 Row: p Column: 12  
 This clone was selected for full length sequencing because it  
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/db_xref="RGD:621012"
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AEVMAVVEEPEPSKSAEDKSPPKRPREAAPGALEMEPAGEREAEEACPFVEEPDQ
AQEQQTPLLEEATEEAVOGLMVGIEIGL"
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## ORIGIN

Query Match 97.6%; Score 966; DB 6; Length 2068;  
Best Local Similarity 98.9%; Pred. No. 1.7e-223;  
Matches 985; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

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Qy	121	GGTGTTCCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTA	180
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Qy	241	GTGGGAGATCGAGCACGACCCTATGGCTGAGGCCTCCCCTTGCTGTGCCCAGATGAGGA	300
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```

## RESULT 2

AC111953

LOCUS AC111953 338115 bp DNA linear HTG 09-NOV-2002

DEFINITION Rattus norvegicus clone CH230-211F3, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 6 unordered pieces.

ACCESSION AC111953

VERSION AC111953.4 GI:24818630

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 338115)

AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,  
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,  
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,  
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,  
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 Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,  
 Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 338115)  
 AUTHORS Worley,K.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-FEB-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 REFERENCE 3 (bases 1 to 338115)  
 AUTHORS Rat Genome Sequencing Consortium.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-NOV-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 COMMENT On Nov 9, 2002 this sequence version replaced gi:23101342.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu

## ----- Project Information

Center project name: GOSJ

Center clone name: CH230-211F3

## ----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 233778 bases at least Q40

Consensus quality: 236747 bases at least Q30

Consensus quality: 238950 bases at least Q20

Estimated insert size: 235437; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 6 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 12369: contig of 12369 bp in length  
 \* 12370 12469: gap of unknown length  
 \* 12470 34481: contig of 22012 bp in length  
 \* 34482 34581: gap of unknown length  
 \* 34582 329483: contig of 294902 bp in length  
 \* 329484 329583: gap of unknown length  
 \* 329584 330973: contig of 1390 bp in length  
 \* 330974 331073: gap of unknown length  
 \* 331074 334003: contig of 2930 bp in length  
 \* 334004 334103: gap of unknown length  
 \* 334104 338115: contig of 4012 bp in length.

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gap	34482. .34581 /estimated_length=unknown
misc_feature	56734. .58848 /note="wgs_contig"
misc_feature	59170. .60297 /note="wgs_contig"
gap	329484. .329583 /estimated_length=unknown
gap	330974. .331073 /estimated_length=unknown
gap	334004. .334103 /estimated_length=unknown

## ORIGIN

Query Match 97.6%; Score 966; DB 12; Length 338115;  
 Best Local Similarity 98.9%; Pred. No. 1.9e-223;  
 Matches 985; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

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Qy	121	GGTGTTCCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCCAAGCACCTTTTTCCTTA	180
Db	117104	GGTGTTCCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCCAAGCACCTTTTTCCTTA	117163
Qy	181	TGAGGAGTCCAAGGAGAGGTTTCGGCAAGCCTAACAAAGAGGCGCGGCTTCAGTGAGGGGCT	240
Db	117164	TGAGGAGTCCAAGGAGAGGTTTCGGCAAGCCTAACAAAGAGGCGCGGCTTCAGTGAGGGGCT	117223
Qy	241	GTGGGAGATCGAGCACGACCCTATGGCTGAGGCCTCCCTTGCTGTGCCAGATGAGGA	300
Db	117224	GTGGGAGATCGAGCACGACCCTATGGTTGAGGCCTCCCTTGCTGTGCCAGATGAGGA	117283
Qy	301	GCAGCTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	360
Db	117284	GCAGCTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	117343
Qy	361	GCCGGAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGA	420
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Qy	421	GAAAGAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAGGAGCCGGA	480
Db	117404	GAAAGAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGA	117463
Qy	481	GCTGGAGCC-----GGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGAGCCCGA	534
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Qy	535	GCCGGAGCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGCCT	594
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Qy	595	CATTGAGGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAAGC	654
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Qy	655	TGAGGTCATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAACA	714
Db	117644	TGAGGTCATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAACA	117703
Qy	715	GCCTCACAGTCCTCCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAGCC	774
Db	117704	GCCTCACAGTCCTCCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAGCC	117763
Qy	775	GGCTGGAGAGCGCGAGGCAGAGGCCTGCCCTTCGTGGAGGAGCCTGACCAAGCCCAGGA	834
Db	117764	GGCTGGAGAGCGCGAGGCAGAGGCCTGCCCTTCGTGGAGGAGCCTGACCAAGCCCAGGA	117823
Qy	835	ACAGCAGACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGG	894
Db	117824	ACAGCAGACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGG	117883
Qy	895	AGAAATCGAAGGCCTGTAGTCACGGTGTCTGTAAAAGAGCCCTCTCTACCCGTTCTGGT	954

Db 117884 AGAAATCGAAGGCCTGTAGTCACGGTGTCTGTAAAAGAGCCCTCTCTACCCGTTCTTGGT 117943

Qy 955 GCCACCTGGCTGTGGCTTGGGAAACCCGCTAGGGCC 990

Db 117944 GCCACCTGGCTGTGGCTTGGGAAACCCGCTAGGGCC 117979

### RESULT 3

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AY061636
LOCUS AY061636 1512 bp mRNA linear ROD 13-NOV-2001
DEFINITION Rattus norvegicus hepatoma-derived apoptotic-related protein mRNA,
complete cds.
ACCESSION AY061636
VERSION AY061636.1 GI:16923254
KEYWORDS .
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1512)
AUTHORS Tirado,O.M., Selva,D.M., Munell,F., Suarez-Quian,C. and Reventos,J.
TITLE A new member of the HDGF family, an apoptotic role?
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1512)
AUTHORS Tirado,O.M., Selva,D.M., Munell,F. and Reventos,J.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2001) URB, Hospitals Vall d'Hebron, Pso Vall
d'Hebron 119-129, Barcelona, Spain
FEATURES
Location/Qualifiers
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/dev_stage="10 weeks old"
CDS 13. .903
/note="HARP; growth factor"
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ORIGIN

Query Match 93.4%; Score 924.4; DB 6; Length 1512;  
Best Local Similarity 97.6%; Pred. No. 2.2e-213;  
Matches 966; Conservative 0; Mismatches 6; Indels 18; Gaps 2;

Qy 1 CGCTATGTCTTGCTTCAGCGCCCCAAAATAACAAGACCGGGGACCTGGTGTTCCAAATT 60  
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Db 9 CGCTATGTCTTGCTTCAGCGCCCCAAAATAACAAGACCGGGGACCTGGTGTTCCAAATT 68

Qy 61 AAAGGGCTATGCCCATTTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCA 120  
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Db 69 AAAGGGCTATGCCCATTTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCA 128

Qy	121	GGTGTTCCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTA	180
Db	129	GGTGTTCCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTA	188
Qy	181	TGAGGAGTCCAAGGAGAGGTTCCGCAAGCCTAACAAAGAGGCGCGGCTTCAGTGAGGGGCT	240
Db	189	TGAGGAGTCCAAGGAGAGGTTCCGCAAGCCTAACAAAGAGGCGCGGCTTCAGTGAGGGGCT	248
Qy	241	GTGGGAGATCGAGCACGACCCCTATGGCTGAGGCCTCCCTTGCTGTGCCAGATGAGGA	300
Db	249	GTGGGAGATCGAGCACGACCCCTATGGTTGAGGCCTCCCTTGCTGTGCCAGATGAGGA	308
Qy	301	GCAGCTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	360
Db	309	GCAGCTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	368
Qy	361	GCCGGAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGA	420
Db	369	GCCGGAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGA	428
Qy	421	GAAAGAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAGGAGCCGGA	480
Db	429	GAAAGAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGA	488
Qy	481	GCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGA	540
Db	489	GCAGGAGCCGGAGCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGA	548
Qy	541	GCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGCCTCATTGA	600
Db	549	G-----CCCAGCCTGCCTATGACCTACTGGAT-----GCCTGGCCTCATTGA	590
Qy	601	GGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAAGCTGAGGT	660
Db	591	GGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAAGCTGAGGT	650
Qy	661	CATGGCTGTAGTGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAACAGCCTCA	720
Db	651	CATGGCTGTAGTGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAACAGCCTCA	710
Qy	721	CAGTCCTCCCAAACGGCCAGGGAGGCGGCGCTGGCGGCTGGAGATGGAGCCGGCTGG	780
Db	711	CAGTCCTCCCAAACGGCCAGGGAGGCGGCGCTGGCGGCTGGAGATGGAGCCGGCTGG	770
Qy	781	AGAGCGCGAGGCAGAGGCCTGCCCCCTTCGTGGAGGAGCCTGACCAAGCCCAGGAACAGCA	840
Db	771	AGAGCGCGAGGCAGAGGCCTGCCCCCTTCGTGGAGGAGCCTGACCAAGCCCAGGAACAGCA	830
Qy	841	GACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGGAGAAAT	900
Db	831	GACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGGAGAAAT	890
Qy	901	CGAAGGCCTGTAGTCACGGTGTCTGTAAAAGAGCCCTCTCTACCCGTTCTGGTGCCACC	960
Db	891	CGAAGGCCTGTAGTCACGGTGTCTGTAAAAGAGCCCTCTCTACCCGTTCTGGTGCCACC	950
Qy	961	TGGCTGTGGCTTGGAACCCGCTAGGGCC	990
Db	951	TGGCTGTGGCTTGGAACCCGCTAGGGCC	980

#### RESULT 4

AF4 58587

LOCUS	AF458587	909 bp	mRNA	linear	PRI 10-JUN-2002
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DEFINITION Homo sapiens hepatoma-derived growth factor HGDF5 mRNA, complete cds.

ACCESSION      AF458587

VERSION AF458587.1 GI:21360801

## KEY WORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 909)

AUTHORS     Zhang, P.Z., Dong, Y.M., Shan, Y.X., Wei, Y.H., Guo, J.H. and Yu, L.

TITLE Direct Submission

JOURNAL Submitted (15-DEC-2001) School of Life Sciences, Institute of Genetics, Fudan University, Handan Road, 220, Shanghai 200433, China

## FEATURES

Location/Qualifiers

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/mol type="mRNA"
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CDS

1. 909

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## ORIGIN

Query Match 91.7%; Score 907.4; DB 5; Length 909;

Best Local Similarity 99.9%; Pred. No. 2.8e-209;

Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ATGTCTTGCTTCAGCCGCCCAAAATACAAGACCGGGGACCTGGTGTTTGCCAAATTAAAG 64

Db 1 ATGTCTTGCTTCAGCCGCCCAAATAACAAGACCGGGGACCTGGTGTGTGCGCAAATTAAAG 60

Qy 65 GGCTATGCCCATTTGGCCAGCGAGGATTGAACATGTCTACTGAACCCAACCGCTACCAGGTG 124

Db 61 GGCTATGCCCATTTGGCCAGCGAGGATTGAACATGTCCTGAACCCAACCGCTACCAGGTG 120

Qy 125 TTCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCCAAGCACCTTTTTCCTTATGAG 184

Db 121 TTCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCCAAGCACCTTTTTCTTATGAG 180

Qy 185 GAGTCCAAGGAGAGGTTTCGGCAAGCCTAACAAGAGGCGCGGCTTCAGTGAGGGGGCTGTGG 244

Db 181 GAGTCCAAGGAGAGGGTTCGGCAAGCCTAACAAGAGGCGCGGCTTCAGTGAGGGGGCTGTGG 240

Qy 245 GAGATCGAGCACGACCCCTATGGCTGAGGCCTCCCCTTGCCTGTGCCAGATGAGGAGCAG 304

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Qy	305	CTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGAGCCG	364
Db	301	CTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGAGCCG	360
Qy	365	GAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGAGAAA	424
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Db	421	GAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAGGAGCCGGAGCTG	480
Qy	485	GAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCCGAGCCCGAGCCGGAGCCG	544
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Qy	605	GAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAAGCTGAGGTCATG	664
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Qy	785	CGCGAGGCAGAGGCCTGCCCCTTCGTGGAGGAGCCTGACCAAGCCCAGGAACAGCAGACT	844
Db	781	CGCGAGGCAGAGGCCTGCCCCTTCGTGGAGGAGCCTGACCAAGCCCAGGAACAGCAGACT	840
Qy	845	CCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGGAGAAATCGAA	904
Db	841	CCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGGAGAAATCGAA	900
Qy	905	GGCCTGTAG	913
Db	901	GGCCTGTAG	909

RESULT 5  
AF458586

LOCUS AF458586 921 bp mRNA linear ROD 24-JUL-2003

DEFINITION Rattus norvegicus hepatoma-derived growth factor variant, mRNA, complete cds.

ACCESSION AF458586

VERSION AF458586.1 GI:33187702

KEYWORDS .

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 921)



AUTHORS Zhang,P.Z., Dong,Y.M., Shan,Y.X., Wei,Y.H., Guo,J.H. and Yu,L.  
TITLE Direct Submission  
JOURNAL Submitted (11-DEC-2001) School of Life Sciences, Intitute of  
Genetics, Fudan University, Handan Road, 220, Shanghai 200433,  
China

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FEATURES             Location/Qualifiers
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ORIGIN

Query Match 89.4%; Score 885.4; DB 6; Length 921;  
Best Local Similarity 98.6%; Pred. No. 6.2e-204;  
Matches 908; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

[illegible]

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Db	481	GAGCCGGAGCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCCGAGCCC	540
Qy	533	GAGCCGGAGCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGC	592
Db	541	GAGCCGGAGCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGC	600
Qy	593	CTCATTGAGGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAA	652
Db	601	CTCATTGAGGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAA	660
Qy	653	GCTGAGGTCATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAA	712
Db	661	GCTGAGGTCATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAA	720
Qy	713	CAGCCTCACAGTCCTCCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAG	772
Db	721	CAGCCTCACAGTCCTCCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAG	780
Qy	773	CCGGCTGGAGAGCGCGAGGCAGAGGCCTGCCCTTCGTGGAGGAGCCTGACCAAGCCCAG	832
Db	781	CCGGCTGGAGAGCGCGAGGCAGAGGCCTGCCCTTCGTGGAGGAGCCTGACCAAGCCCAG	840
Qy	833	GAACAGCAGACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTT	892
Db	841	GAACAGCAGACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTT	900
Qy	893	GGAGAAATCGAAGGCCTGTAG	913
Db	901	GGAGAAATCGAAGGCCTGTAG	921

LOCUS (LOC): AF458587 GenBank (R)  
 GenBank ACC. NO. (GBN): AF458587  
 GenBank VERSION (VER): AF458587.1 GI:21360801  
 CAS REGISTRY NO. (RN): 430805-71-3  
 SEQUENCE LENGTH (SQL): 909  
 MOLECULE TYPE (CI): mRNA; linear  
 DIVISION CODE (CI): Primates  
 DATE (DATE): 10 Jun 2002  
 DEFINITION (DEF): Homo sapiens hepatoma-derived growth factor HGDF5 mRNA, complete cds.  
 SOURCE: human.  
 ORGANISM (ORGN): Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
 Hominidae; Homo  
 NUCLEIC ACID COUNT (NA): 209 a 245 c 331 g 124 t  
 REFERENCE: 1 (bases 1 to 909)  
 AUTHOR (AU): Zhang,P.Z.; Dong,Y.M.; Shan,Y.X.; Wei,Y.H.; Guo,J.H.; Yu,L.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (15-DEC-2001) School of Life Sciences,  
 Institute of Genetics, Fudan University, Handan Road,  
 220, Shanghai 200433, China

# FEATURES (FEAT):

Feature Key	Location	Qualifier
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841 ccgttggaag aagaggccac agaggaggca gtccaggggc tgatgggttg agaaatcgaa
  
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901 ggctgtag

<!--StartFragment--> GenCore version 5.1.9  
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 22, 2006, 19:06:45 ; Search time 750 Seconds  
 (without alignments)  
 9203.368 Million cell updates/sec

Title: US-10-501-053-1  
 Perfect score: 990  
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Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
 1: geneseqn1980s:\*  
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 3: geneseqn2000s:\*  
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 5: geneseqn2001bs:\*  
 6: geneseqn2002as:\*  
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 13: geneseqn2004bs:\*  
 14: geneseqn2005s:\*  
 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	990	100.0	990	9	ADA37366	Ada37366 Human hep
2	885.4	89.4	921	11	ADQ96711	Adq96711 Human Wol
3	511.8	51.7	861	11	ADO59824	Ado59824 Human hep
4	505.2	51.0	882	2	AAV01730	Aav01730 Mouse liv
5	347.8	35.1	783	2	AAV57582	Aav57582 Nucleus-t
6	226.8	22.9	880	4	AAF30641	Aaf30641 Human hep
7	223.8	22.6	756	4	AAD16358	Aad16358 Human sbg

	8	223.8	22.6	794	12	ACH91708	Ach91708 Human gen
c	9	154	15.6	30191	12	ADQ97654	Adq97654 Mouse can
	10	148	14.9	2779	12	ADJ75971	Adj75971 Marker ge
	11	141.8	14.3	110000	14	ADZ12814_2	Continuation (3 of
	12	138.4	14.0	1744	15	AEF36279	Aef36279 Hepatoma-
c	13	138.4	14.0	247461	13	ABD33153	Abd33153 Murine ca
	14	137.8	13.9	714	2	AAT88420	Aat88420 Mouse hep
	15	137.8	13.9	1563	2	AAV03867	Aav03867 Mouse hep
	16	135	13.6	723	2	AAQ79903	Aaq79903 Human hep
	17	135	13.6	723	10	ADF10208	Adf10208 Human hep
	18	135	13.6	732	3	AAA40112	Aaa40112 Human HDG
	19	135	13.6	834	3	AAA40117	Aaa40117 Human HDG
	20	135	13.6	1386	5	AAF59292	Aaf59292 Human hHD
	21	135	13.6	2133	3	AAF18049	Aaf18049 Lung canc
	22	135	13.6	2219	12	ADQ83188	Adq83188 Human tum
	23	135	13.6	2219	12	ADQ84369	Adq84369 Human tum
	24	135	13.6	2219	13	ADQ85101	Adq85101 Human tum
	25	135	13.6	2219	13	ADQ83876	Adq83876 Human tum
	26	135	13.6	2219	13	ADQ86291	Adq86291 Human tum
	27	135	13.6	2219	13	ACN37480	Acn37480 Tumour-as
	28	135	13.6	2376	2	AAQ79902	Aaq79902 Human hep
	29	135	13.6	2376	3	AAA40118	Aaa40118 Human HDG
	30	135	13.6	2376	5	ABA83087	Aba83087 Hepatoma-
	31	135	13.6	2376	10	ADF10210	Adf10210 Human hep
	32	135	13.6	2376	10	ADK61214	Adk61214 Ovarian c
	33	135	13.6	2376	12	ADJ45234	Adj45234 Human hep
	34	135	13.6	2376	13	ADR25187	Adr25187 Breast ca
	35	135	13.6	2376	14	ADY14323	Ady14323 DNA encod
	36	135	13.6	2376	14	ADZ48952	Adz48952 Insulin s
	37	135	13.6	2376	15	AEE60970	Aee60970 Human pat
	38	135	13.6	2388	14	AED73424	Aed73424 Human pla
	39	133.4	13.5	2135	10	ADE31258	Ade31258 Human dia
	40	132	13.3	480	9	ACH45232	Ach45232 Human foe
	41	128.2	12.9	869	2	AAV39154	Aav39154 Lung grow
	42	127	12.8	1926	3	AAA50254	Aaa50254 Epstein B
	43	127	12.8	1926	4	AAF82902	Aaf82902 EBV tethe
	44	127	12.8	1926	10	ADK65580	Adk65580 Human her
	45	127	12.8	1926	14	ADV68155	Adv68155 Epstein-B

## ALIGNMENTS

## RESULT 1

ADA37366

ID ADA37366 standard; cDNA; 990 BP.

XX

AC ADA37366;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human hepatoma-derived growth factor 5 cDNA.

XX

KW ds; gene; cytostatic; antiinflammatory; gene therapy; human;

KW hepatoma-derived growth factor 5; HDGF5; diagnosis; malignant tumour;

KW surgical efficiency; liver cancer; hepatitis; inflammation.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 5..913

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FT          /*tag= a
FT          /product= "Human hepatoma-derived growth factor 5"
XX
PN WO2003057883-A1.
XX
PD 17-JUL-2003.
XX
PF 02-JAN-2003; 2003WO-CN000003.
XX
PR 11-JAN-2002; 2002CN-00110535.
XX
PA (YULL/) YU L.
XX
PI Yu L, Tang L, Guo Z, Zhang P, Dong Y;
XX
DR WPI; 2003-587131/55.
DR P-PSDB; ADA37367.
XX
PT Human hepatoma-derived growth factor 5 and encoded polynucleotide,
PT applicable in early diagnosis of malignant tumor, and development of
PT drugs for hepatitis and acute inflammatory in various organs.
XX
PS Claim 1; Page 10; 26pp; Chinese.
XX
CC The invention relates to an isolated DNA encoding a human hepatoma-
CC derived growth factor 5 (HDGF5), or sequences that have at least 70 %
CC homology to the HDGF5 sequence. The polynucleotide and its encoded
CC polypeptide are applicable in early diagnosis of malignant tumours,
CC monitoring surgical efficiency and prognosis of liver cancer, and
CC development of drugs for hepatitis and acute inflammation in various
CC organs. This sequence represents the human HDGF5 cDNA.
XX
SQ Sequence 990 BP; 221 A; 273 C; 354 G; 142 T; 0 U; 0 Other;

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Query Match 100.0%; Score 990; DB 9; Length 990;  
Best Local Similarity 100.0%; Pred. No. 7.9e-176;  
Matches 990; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	AAAGGGCTATGCCCATTTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCA	120
Db	61	AAAGGGCTATGCCCATTTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCA	120
Qy	121	GGTGTTCCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTA	180
Db	121	GGTGTTCCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTA	180
Qy	181	TGAGGAGTCCAAGGAGAGGTTCGGCAAGCCTAACAAGAGGCGCGGCTTCAGTGAGGGGCT	240
Db	181	TGAGGAGTCCAAGGAGAGGTTCGGCAAGCCTAACAAGAGGCGCGGCTTCAGTGAGGGGCT	240
Qy	241	GTGGGAGATCGAGCACGACCCTATGGCTGAGGCCTCCCCTTGCTGTGCCCAGATGAGGA	300
Db	241	GTGGGAGATCGAGCACGACCCTATGGCTGAGGCCTCCCCTTGCTGTGCCCAGATGAGGA	300
Qy	301	GCAGCTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	360
Db	301	GCAGCTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	360

Qy	361	GCCGGAATCCAGGCCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGA	420
Db	361	GCCGGAATCCAGGCCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGA	420
Qy	421	GAAAGAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAGGAGCCGGA	480
Db	421	GAAAGAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAGGAGCCGGA	480
Qy	481	GCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCCGAGCCCGAGCCGGA	540
Db	481	GCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCCGAGCCCGAGCCGGA	540
Qy	541	GCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGCCTCATTGA	600
Db	541	GCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGCCTCATTGA	600
Qy	601	GGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAAGCTGAGGT	660
Db	601	GGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAAGCTGAGGT	660
Qy	661	CATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAACAGCCTCA	720
Db	661	CATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAACAGCCTCA	720
Qy	721	CAGTCCTCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAGCCGGCTGG	780
Db	721	CAGTCCTCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAGCCGGCTGG	780
Qy	781	AGAGCGCGAGGCAGAGGCCTGCCCCTTCGTGGAGGAGCCTGACCAAGCCCAGGAACAGCA	840
Db	781	AGAGCGCGAGGCAGAGGCCTGCCCCTTCGTGGAGGAGCCTGACCAAGCCCAGGAACAGCA	840
Qy	841	GACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGGAGAAAT	900
Db	841	GACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGGAGAAAT	900
Qy	901	CGAAGGCCTGTAGTCACGGTGTCTGTAAAAGAGCCCTCTCTACCCGTTCTGGTGCCACC	960
Db	901	CGAAGGCCTGTAGTCACGGTGTCTGTAAAAGAGCCCTCTCTACCCGTTCTGGTGCCACC	960
Qy	961	TGGCTGTGGCTTGGGAAACCCGCTAGGGCC	990
Db	961	TGGCTGTGGCTTGGGAAACCCGCTAGGGCC	990

## RESULT 2

ADQ 96 711

ID ADQ96711 standard; cDNA; 921 BP.

XX

AC ADQ96711;

XX

DT 23-SEP-2004 (first entry)

XX

DE Human Wolf-Hirschhorn syndrome-related protein (WHSRP) cDNA.

XX

KW Wolf-Hirschhorn syndrome-related protein; WHSRP; cell differentiation;  
KW development; human; ss; gene.

XX

OS Homo sapiens.

XX



FH Key Location/Qualifiers  
 FT CDS 1. .921  
 FT /\*tag= a  
 FT /product= "Human Wolf-Hirschhorn syndrome-related protein  
 FT (WHSRP)"  
 XX  
 PN CN1376796-A.  
 XX  
 PD 30-OCT-2002.  
 XX  
 PF 04-APR-2002; 2002CN-00111267.  
 XX  
 PR 04-APR-2002; 2002CN-00111267.  
 XX  
 PA (UYFU-) UNIV FUDAN.  
 XX  
 PI Yu L, Tang L, She X;  
 XX  
 DR WPI; 2003-202161/20.  
 DR P-PSDB; ADQ96712.  
 XX  
 PT Coding sequence of novel human protein and its preparing process and  
 PT application.  
 XX  
 PS Claim 1; SEQ ID NO 1; 17pp; Chinese.  
 XX  
 CC The invention relates to a novel cDNA sequence for the human Wolf-  
 CC Hirschhorn syndrome-related protein (hWHSRP) which is associated with  
 CC human cell differentiation and development and the encoded polypeptide,  
 CC in addition to a process for preparing and applying the said  
 CC polynucleotide and polypeptide sequences. The current sequence is that of  
 CC the human WHSRP cDNA of the invention.  
 XX  
 SQ Sequence 921 BP; 212 A; 248 C; 337 G; 124 T; 0 U; 0 Other;

Query Match 89.4%; Score 885.4; DB 11; Length 921;  
 Best Local Similarity 98.6%; Pred. No. 2.8e-156;  
 Matches 908; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

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Db	1	ATGTCTTGCTTCAGCCGCCCAAAATACAAGACCGGGGACCTGGTGTGTTGCCAAATTAAAG	60
Qy	65	GGCTATGCCCATTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCAGGTG	124
Db	61	GGCTATGCCCATTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCAGGTG	120
Qy	125	TTCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCCAAGCACCTTTTTCCTTATGAG	184
Db	121	TTCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCCAAGCACCTTTTTCCTTATGAG	180
Qy	185	GAGTCCAAGGAGAGGTTCGGCAAGCCTAACAAGAGGCGCGGCTTCAGTGAGGGGCTGTGG	244
Db	181	GAGTCCAAGGAGAGGTTCGGCAAGCCTAACAAGAGGCGCGGCTTCAGTGAGGGGCTGTGG	240
Qy	245	GAGATCGAGCACGACCCTATGGCTGAGGCCTCCCCTTGCTGTGCCAGATGAGGAGCAG	304
Db	241	GAGATCGAGCACGACCCTATGGTTGAGGCCTCCCCTTGCTGTGCCAGATGAGGAGCAG	300
Qy	305	CTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGAGCCG	364

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Db      301 CTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGAGCCG 360
Qy      365 GAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGAGAAA 424
      |||
Db      361 GAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGAGAAA 420
Qy      425 GAGTGT-----GAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAG 472
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Db      421 GAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAG 480
Qy      473 GAGCCGGAGCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGAGCCC 532
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Db      481 GAGCCGGAGCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGAGCCC 540
Qy      533 GAGCCGGAGCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGC 592
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Db      541 GAGCCGGAGCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGC 600
Qy      593 CTCATTGAGGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAA 652
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Db      601 CTCATTGAGGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAA 660
Qy      653 GCTGAGGTCATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAA 712
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Db      661 GCTGAGGTCATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAA 720
Qy      713 CAGCCTCACAGTCCTCCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAG 772
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Db      721 CAGCCTCACAGTCCTCCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAG 780
Qy      773 CCGGCTGGAGAGCGCGAGGCAGAGGCCTGCCCTTCGTGGAGGAGCCTGACCAAGCCCAG 832
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Db      781 CCGGCTGGAGAGCGCGAGGCAGAGGCCTGCCCTTCGTGGAGGAGCCTGACCAAGCCCAG 840
Qy      833 GAACAGCAGACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTT 892
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Db      841 GAACAGCAGACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTT 900
Qy      893 GGAGAAATCGAAGGCCTGTAG 913
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Db      901 GGAGAAATCGAAGGCCTGTAG 921
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